SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Levy, Gary
                   Clark, David A.

    (ii) TITLE OF INVENTION: Methods of Modulating Immune Coagulation

    (iii) NUMBER OF SEQUENCES: 4

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: BERESKIN & PARR
        (B) STREET: 40 King Street West
        (C) CITY: Toronto
        (D) STATE: Ontario
        (E) COUNTRY: Canada
        (F) ZIP: M5H 3Y3

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: 09/442,143
        (B) FILING DATE: 15-NOV-1999
        (C) CLASSIFICATION:

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Gravelle, Micheline
        (B) REGISTRATION NUMBER: 40,261
        (C) REFERENCE/DOCKET NUMBER: 9579-014

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (416) 364-7311
        (B) TELEFAX: (416) 361-1398

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4630 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo sapiens

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GATCTAGGGT TGGAAGCCAG GTCTCCTGAG TATGCGAGAA TAAATACAGT CATGGAAGTG        60

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ACAGAAAAGT CATAGGAAAT CAGGTTAAAG ACATAAATAT GAGATAGGCT ACAGAGTGTT       180

TTAAGTAATA CAATAAAACA TTTAGATTTT TGCCCATGTC AGTCATTTTG AAATTATTTT       240

TAAAGCAAAA AAACCCTTTT TAAACAAGAA ATCTTATGAG ATGTCAATAT GCAAAACAAA       300

TTAAAAGGAG GTGGTTTCTC TAACTGAAGC TGTTCCTCTT TCCTGCCTTC AGCCTCTGAA       360
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CACTGGCATA GCTCAAAGAT TCACATTTGA GCAGCTGTGG AAGATGACAG TACAATTACC    600

AAAATGTCGA AGGGCAAAGG AGGCAGCTAC TGGTTTTGAT GAAAGACAAT TATGTCCTTT    660

TAAATGGGTC TTAGACATTT AGACATTTAT ATACACTATG CTACGGACAA AGGAATAGAA    720

AGTAGCACTT TTTTCTCCAC TAGTTTTCTT CTCTTTTTCA AGTAGATGAA GCAAAAGTCA    780

ACTGCAATAG TCAGAAAGCT GTACTTTGTT ACACTTAGAA ACTTCTAAAA GTGCTTAAGA    840

TTTCACCTGA AAGTCCAACA TGAAGAAAAT ACAGGCTCCC CAATGCCCCA TTCTAAGAAG    900

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TCTTGCCACT TACGGTTTTT TGGTTGTGGC AAACAATGAA ACAGAGGAAA TTAAAGATGA   1440

AAGAGCAAAG GATGTCTGCC CAGTGAGACT AGAAAGCAGA GGGAAATGCG AAGAGGCAGG   1500

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ACTGTTGTTA CCCAGTACAG GAGCCCCGGG AGAGGTTGGT GATAACAGAG TTAGAGAATT   1740

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TTACTAAACA CCTTCAAGTA AGTTTAGTAA AGTTTCATTA CTGCCATTGA TTCAATTATC   2340
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TAGCTTTGAA GTTTACTGTG ACATGGAGAC CATGGGGGGA GGCTGGACAG TGCTGCAGGC      2580

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TTCAGGCTGG TGGTTTGATG CATGTCTTTC TGCAAACTTA AATGGCAAAT ATTATCACCA      3000

AAAATACAGA GGTGTCCGTA ATGGGATTTT CTGGGGTACC TGGCCTGGTG TAAGTGAGGC      3060

ACACCCTGGT GGCTACAAGT CCTCCTTCAA AGAGGCTAAG ATGATGATCA GACCCAAGCA      3120

CTTTAAGCCA TAAATCACTC TGTTCATTCC TCCAGGTATT CGTTATCTAA TAGGGCAATT      3180

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ATGCTGTTAT CCAATGAACA CTTGCAAGCA ATTAGCAATA TTGAGAATTA TACATTAGAT      3360

TTACAATTCT TTTAATTTCT ATTGAAACTT TTTCTATTGC TTGTATTACT TGCTGTATTT      3420

AAAAAATAAT TGTTGGCTGG GTGTGGTAGC TCACGCCTGT AATCCCAGCA CTTTGGAATG      3480

TCAAGGCAGG CAGATCACTT GAGGTCAGGA GTTTGAGACC AGCCTGGCCA AACATGTGAA      3540

ACGCTGTCTC TATTAAAAAT ACAAAAATTA GCCGGGCATG GTGGTACATG CCTGTAATCA      3600

ACGCTGTTTA TTAAAAATAC AAAAATTAGC CGGGCATGGT GGACATGCCT GTAATCCTAG      3660

TACTTGGGAG GCTGAGGCAG GAGAATCGCT TGAACCTGAG AGGAAGAGGT TGCAGTGAGC      3720

CAAGAATGAG CCACTGCACT CCAGCATGGG TGACAGAGAA AACTCTGTCT CAAACAAAAA      3780

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TTTAAGCACA TCTGAAGGTA TATCACTCTT TTCAGGCTAT AATTATTTGG GTAATCTTCA      3900

TTCTGAGACA AACTTAATCT ATATCATTTA CTTTGCAACA GAACAACCCT ACAGCATTTT      3960

GGTTCCCAGA CTAAGGGAAC TAATATCTAT ATAATTAAAC TTGTTCATTT ATCATTCATG      4020

AAATATAAAA TACTTGTCAT TTAAACCGTT TAAAAATGTG GTAGCATAAT GTCACCCCAA      4080

AAAGCATTCA GAAAGCAATG TAACTGTGAA GACCAGGGTT TAAAGGTAAT TCATTTATAG      4140

TTTATAACTC CTTAGATGTT TGATGTTGAA AACTGCTTTA ACATGAAAAT TATCTTCCTC      4200

TGCTCTGTGT GAACAATAGC TTTTAATTTA AGATTGCTCA CTACTGTACT AGACTACTGG      4260

TAGGTTTTTT TGGGGGGGGG TGGGTAGGGA TATGTGGGTA ATGAAGCATT TACTTACAGG      4320
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CTATCATACT CTGAGGCCAA TTTTATCTCC AAAGCAATAA TATCATTAAG TGATTCACTT    4380

CATAGAAGGC TAAGTTTCTC TAGGACAGAT AGAAACATG AATTTTGAAA TATATAGAAC      4440

AGTAGTTAAA ATACTATATA TTTCAACCCT GGCTGGTAGA TTGCTTATTT TACTATCAGA     4500

AACTAAAAGA TAGATTTTTA CCCAAACAGA AGTATCTGTA ATTTTTATAA TTCATCAATT     4560

CTGGAATGCT ATATATAATA TTTAAAAGAC TTTTTAAATG TGTTTAATTT CATCATCGTA     4620

AAAAGGGATC                                                            4630
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(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 439 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Lys Leu Ala Asn Trp Tyr Trp Leu Ser Ser Ala Val Leu Ala Thr
1               5                   10                  15

Tyr Gly Phe Leu Val Val Ala Asn Asn Glu Thr Glu Glu Ile Lys Asp
            20                  25                  30

Glu Arg Ala Lys Asp Val Cys Pro Val Arg Leu Glu Ser Arg Gly Lys
        35                  40                  45

Cys Glu Glu Ala Gly Glu Cys Pro Tyr Gln Val Ser Leu Pro Pro Leu
    50                  55                  60

Thr Ile Gln Leu Pro Lys Gln Phe Ser Arg Ile Glu Glu Val Phe Lys
65                  70                  75                  80

Glu Val Gln Asn Leu Lys Glu Ile Val Asn Ser Leu Lys Lys Ser Cys
            85                  90                  95

Gln Asp Cys Lys Leu Gln Ala Asp Asp Asn Gly Asp Pro Gly Arg Asn
            100                 105                 110

Gly Leu Leu Leu Pro Ser Thr Gly Ala Pro Gly Glu Val Gly Asp Asn
            115                 120                 125

Arg Val Arg Glu Leu Glu Ser Glu Val Asn Lys Leu Ser Ser Glu Leu
    130                 135                 140

Lys Asn Ala Lys Glu Glu Ile Asn Val Leu His Gly Arg Leu Glu Lys
145                 150                 155                 160

Leu Asn Leu Val Asn Met Asn Asn Ile Glu Asn Tyr Val Asp Ser Lys
                165                 170                 175

Val Ala Asn Leu Thr Phe Val Val Asn Ser Leu Asp Gly Lys Cys Ser
            180                 185                 190

Lys Cys Pro Ser Gln Glu Gln Ile Gln Ser Arg Pro Val Gln His Leu
            195                 200                 205

Ile Tyr Lys Asp Cys Ser Asp Tyr Tyr Ala Ile Gly Lys Arg Ser Ser
    210                 215                 220
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Glu Thr Tyr Arg Val Thr Pro Asp Pro Lys Asn Ser Ser Phe Glu Val
225                 230             235                 240

Tyr Cys Asp Met Glu Thr Met Gly Gly Gly Trp Thr Val Leu Gln Ala
            245             250                 255

Arg Leu Asp Gly Ser Thr Asn Phe Thr Arg Thr Trp Gln Asp Tyr Lys
            260             265             270

Ala Gly Phe Gly Asn Leu Arg Arg Glu Phe Trp Leu Gly Asn Asp Lys
        275             280             285

Ile His Leu Leu Thr Lys Ser Lys Glu Met Ile Leu Arg Ile Asp Leu
    290             295             300

Glu Asp Phe Asn Gly Val Glu Leu Tyr Ala Leu Tyr Asp Gln Phe Tyr
305             310             315             320

Val Ala Asn Glu Phe Leu Lys Tyr Arg Leu His Val Gly Asn Tyr Asn
            325             330             335

Gly Thr Ala Gly Asp Ala Leu Arg Phe Asn Lys His Tyr Asn His Asp
        340             345             350

Leu Lys Phe Phe Thr Thr Pro Asp Lys Asp Asn Asp Arg Tyr Pro Ser
    355             360             365

Gly Asn Cys Gly Leu Tyr Tyr Ser Ser Gly Trp Trp Phe Asp Ala Cys
    370             375             380

Leu Ser Ala Asn Leu Asn Gly Lys Tyr Tyr His Gln Lys Tyr Arg Gly
385             390             395             400

Val Arg Asn Gly Ile Phe Trp Gly Thr Trp Pro Gly Val Ser Glu Ala
            405             410             415

His Pro Gly Gly Tyr Lys Ser Ser Phe Lys Glu Ala Lys Met Met Ile
            420             425             430

Arg Pro Lys His Phe Lys Pro
            435
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(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 5403 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CATAAGGCGT GTCTGACAAA TTCTTCATAC ACACATTTCC CCTTTGCACA TTCAGTCTGT        60

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TGAAGGCTCA GCAAAGCCAA TACGTGTTAT GTCCAGTTGG AGACAGTGCC AGGGCCAACA       180

TTCCAGACTT CTCAGATAGA AAGTGCGCCT GCCTGCCCTG CTCTGAGAAT TTGAAGAGAG       240

TAGTTCAGTT AGAATTAAGA GGCAGTAGAG AAAAGTCTTG GGAAATCTGG TTAGAGATAT       300

AAATATGAGA ACTGGACATG GTGGTACACA CCTGTGATCT CTGTGTTTAG GAGGGAGAGG       360
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CAGAGAGATC AGGAGTTCAA GGCCAGCCTG AGCTACTTGA GACCCAGTCT AAATAAATAA      420

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CAGTATGCAC AATGAACTTA AGAGAGACCC CCAGCTCCTG AGCTGAGTGA TGGGGAAGGA      600

CAGCCACTGC CTGTGATGTG TGAGTGACGT GCTTCCAAGT GTTTTAACCA CTGACGATTA      660

CATAGCCTGC ACAGTCAGGA GAAAACAGCC GTATTCTCTG CCAGTTCTCT TCCCTTTTAC      720

AAACAGATGA GAGACACACA CAGAGAATCC ATTTAAAGAG CGGACCTTTG TTCTGATTAG      780

GGGCAATTTT AAGTACTTAA GAGTTCACAC AAAGTCTAGC CTTCAAAAAG AAAACAGGTT      840

CCCAAACTAG GGAGGAAACA GAATCATTTC CATTTTGGTG ACATTTAGTG GGAAGAAGCT      900

CACAGACATT TAGACGTTCC AACTCTTTCC CCACTAGTGG ACCAAGTATA TAATATGGTA      960

TCTTTTGGGC ACTGGTATTA CAACTGTTTT TTAAACAAAA GACTTTCCTT GTGCTTTACT     1020

AAAAACCCAG ACGGTGAATC TTGAATACAA TGCGTGGCAC CCACGGCAGG CATTCTATTG     1080

TGCATAGTTT TGACTGACAG GAGATGACAG CATTTGGCTG GCTGCGCTTG CTGAGGACCC     1140

TCTCCTCCTG TGTGGCGTCT GAGACTGTGA TGCAAATGCG CCCGCCCTTT TCTGGGAACT     1200

CAGAACGCCT GAGTCAGGCG GCGGTGGCTA TTAAAGCGCC TGGTCAGGCT GGGCTGCCGC     1260

ACTGCAAGGA TGAGGCTTCC TGGTTGGTTG TGGCTGAGTT CTGCCGTCCT CGCTGCCTGC     1320

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GCCGAGGACA GTAGAGTCCA GGAACTGGAG AGTCAGGTGA ACAAGCTGTC CTCAGAGCTG     1680

AAGAATGCAA AGGACCAGAT CCAGGGGCTG CAGGGGCGCC TGGAGACGCT CCATCTGGTA     1740

AATATGAACA ACATTGAGAA CTACGTGGAC AACAAAGTGG CAAATCTAAC CGTTGTGGTC     1800

AACAGTTTGG ATGGCAAGTG TTCCAAGTGT CCCAGCCAAG AACACATGCA GTCACAGCCG     1860

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GAGAAACAAG TGTTTTCTCA AATGAGACAA CAGAAATGGT AAATGATCCA CGTACAAAAA     2040

TCCTATTAGT TGTACTCGTT AGAGACCGTC ACTTGCAAGT CTCTAGACCT TCCCTGCTAG     2100

GTCGACCAAC AGACGAGCAG AAACAGATTC CTCCCGGAAT CTGAACACAT ATTTGAACAC     2160

AGGACAGGTA TGGCAAGGTT CCTGGCTCTG CTTGCTTAGG TCCCTGGGAA TCAGATCTTG     2220

GGTGGCTGAT GGGCTTTATA AGGCTTTCAC AAACAATCTG CTGTGCTAGG TTCTCAAATA     2280

TCTAGTGAGA ATGGGAGATT TTTATACATG GAAGCATCTC TCCTCTCTCT CTCCTCTCTC     2340
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GAACTTCGGG GGTTGAGACT TAGTGCATAT GCATCCTCAC CATTCCAGTT AGTGAATGTT   2520
AACACTATTT AAGGTCACAG ACCTAACAGC CTTCTGTGTC CGGATTCCTG GATTCCTAGG   2580
ACCTTTGTGG ATGGGTTGCC ACACCCTCTG TGTTCATCCT GACTGTGAGG TCGATGGGAC   2640
ATAGTAGGGA TAACTTTCAT TTGGAATCTC TAGAGATGGT AGGTCATCAT GTCATAGAAT   2700
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GAATCTTATA TTGAACTTTC TTTACCTGAC TCAAATTTTA TTAAAATTAA CTGGGAACAA   2940
ATAGTTGGTC TCTAATCTCT ACAAAAACCA CCAAATGATT ACACTGAGCA TAATTATAAT   3000
CACCCTGCTG CTACGTCTAG AAACCAAACT GTGAAATATT GGCTGACTGT ATACCTTCCT   3060
AAATAATAAA TTCAGGATAA CATTGCCATA TTATTGGAGA ACCCCCCCCT CCCTTTTAAA   3120
ACTGGAATCA TTTTATGTCA ATCTCAGGTG AAATACGAAT GGGTTTCAGA ACAGTGCTGT   3180
GCACTGAAGG CTGACATTTA GAACATATAT AACGATTTCT GTAAAGTCTG CTGTAACAAT   3240
TGCTGATTGT ATCCTAGGAG ACTTGGACTC CTCTCAACGT TAAGGCAGAG GAATATAATG   3300
GTTATGAGAG TAAAACTCTC TGTCAGGTAC ATCTGGCTTT CTGTCCCAGC TCTGTCACTT   3360
AACACTTAGT TGCGGTGGGA AAACTCCCTG ATCTTCCGGG AGACTAAGTA ACTGTATAAG   3420
CAAGCTGGCC GTGATATCCA CGTCGTAAGG CTGCTGTGTG GGTTCAGTGA AAACTGTTAC   3480
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TTACTACTCT TTGCTGTTAG TGTTGCCACC AGGATTGCCA TTCAAGGCAG TCCTGTATAC   3600
TTGATAACAC CAGTTGGTTC TGAGGCCTTA GTTAGCATCT GTTAGCCTGG TTCAGGAGAG   3660
TGTATCAGAG CCAGGTTCCT CTATCACATA AACTGTAACG CAAGTGAATT GTCCAATTGC   3720
TGTTGAGTCT GAGAGTCCTT GAGGTGCATA GCTTTGACTA ATAAATCCCC ATGCTTTTAT   3780
GCTTTTCCTT CCTCCCTCTT CCAGTTCAAC ATCTAATATA CAAAGATTGT TCCGACCACT   3840
ACGTGCTAGG AAGGAGAAGC AGTGGGGCCT ACAGAGTTAC CCCTGATCAC AGAAACAGCA   3900
GCTTTGAGGT CTACTGTGAC ATGGAGACCA TGGGTGGAGG CTGGACGGTG CTGCAGGCTC   3960
GCCTTGATGG CAGCACCAAC TTCACCAGAG AGTGGAAAGA CTACAAAGCC GGCTTTGGAA   4020
ACCTTGAACG AGAATTTTGG TTGGGCAACG ATAAAATTCA TCTTCTGACC AAGAGTAAGG   4080
AAATGATTTT GAGAATAGAT CTTGAAGACT TTAATGGTCT CACACTTTAT GCCTTGTATG   4140
ATCAGTTTTA TGTGGCTAAT GAATTCTCA ATACCGATT ACACATCGGT AACTACAATG   4200
GCACGGCAGG GGATGCCTTG CGTTTCAGTC GACACTACAA CCATGACCTG AGGTTTTTCA   4260
CAACCCCAGA CAGAGACAAC GATCGGTACC CCTCTGGGAA CTGTGGGCTC TATTACAGCT   4320
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AGCCAGGTGG CTACAAGTCC TCCTTCAAAC AGGCCAAGAT GATGATTAGG CCCAAGAATT    4500

TCAAGCCATA AATTGCTAGT GTTCATCTCT CTGGGCACTC ACTATCTAAG AGGACGATGA    4560

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CAAAACCTTT CATTTTTATT AGTTGAAAAG TTTCCTAATA TTTTTATTAT TTTTATAATA    4800

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AAAATAATGT TACCCTGTAG ACTTTGGTTT AGTGGTAATT CACTTACTGT TTATAGCCTG    5160

TTAGACCGCG ATACAAAGC TGCTTTATCC TCTCCCTCTG CTCTCTGTGC ACAATGGTTT    5220

GTGATGTAAG GTGCTAGACT ACTGTAAGGT TTCCTTGGGG AAAGGCATGG TAAGGGAAAA    5280

CACACTGGTT TATATTTTGA AAGCCAATCC TAATCCCAAA GCAATACTGT TGTCGAGGAG    5340

TCAACGTTCT AGGAAGCTGA CTTTTCTAGA ACAAATGTAT TTATTAGGAT GAATTTGGGA    5400

ATT                                                                  5403
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(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 432 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Arg Leu Pro Gly Trp Leu Trp Leu Ser Ser Ala Val Leu Ala Ala
1               5                   10                  15

Cys Arg Ala Val Glu Glu His Asn Leu Thr Glu Gly Leu Glu Asp Ala
            20                  25                  30

Ser Ala Gln Ala Ala Cys Pro Ala Arg Leu Glu Gly Ser Gly Arg Cys
        35                  40                  45

Glu Gly Ser Gln Cys Pro Phe Gln Leu Thr Leu Pro Thr Leu Thr Ile
    50                  55                  60

Gln Leu Pro Arg Gln Leu Gly Ser Met Glu Glu Val Leu Lys Glu Val
65                  70                  75                  80
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Arg Thr Leu Lys Glu Ala Val Asp Ser Leu Lys Lys Ser Cys Gln Asp
            85                      90                      95

Cys Lys Leu Gln Ala Asp Asp His Arg Asp Pro Gly Gly Asn Gly Gly
            100                     105                 110

Asn Gly Ala Glu Thr Ala Glu Asp Ser Arg Val Gln Glu Leu Glu Ser
        115                     120                 125

Gln Val Asn Lys Leu Ser Ser Glu Leu Lys Asn Ala Lys Asp Gln Ile
    130                 135                 140

Gln Gly Leu Gln Gly Arg Leu Glu Thr Leu His Leu Val Asn Met Asn
145                 150                 155                     160

Asn Ile Glu Asn Tyr Val Asp Asn Lys Val Ala Asn Leu Thr Val Val
                165                 170                 175

Val Asn Ser Leu Asp Gly Lys Cys Ser Lys Cys Pro Ser Gln Glu His
            180                 185                 190

Met Gln Ser Gln Pro Val Gln His Leu Ile Tyr Lys Asp Cys Ser Asp
            195                 200                 205

His Tyr Val Leu Gly Arg Arg Ser Ser Gly Ala Tyr Arg Val Thr Pro
    210                 215                 220

Asp His Arg Asn Ser Ser Phe Glu Val Tyr Cys Asp Met Glu Thr Met
225                 230                 235                     240

Gly Gly Gly Trp Thr Val Leu Gln Ala Arg Leu Asp Gly Ser Thr Asn
                245                 250                 255

Phe Thr Arg Glu Trp Lys Asp Tyr Lys Ala Gly Phe Gly Asn Leu Glu
            260                 265                 270

Arg Glu Phe Trp Leu Gly Asn Asp Lys Ile His Leu Leu Thr Lys Ser
            275                 280                 285

Lys Glu Met Ile Leu Arg Ile Asp Leu Glu Asp Phe Asn Gly Leu Thr
    290                 295                 300

Leu Tyr Ala Leu Tyr Asp Gln Phe Tyr Val Ala Asn Glu Phe Leu Lys
305                 310                 315                     320

Tyr Arg Leu His Ile Gly Asn Tyr Asn Gly Thr Ala Gly Asp Ala Leu
            325                 330                 335

Arg Phe Ser Arg His Tyr Asn His Asp Leu Arg Phe Phe Thr Thr Pro
            340                 345                 350

Asp Arg Asp Asn Asp Arg Tyr Pro Ser Gly Asn Cys Gly Leu Tyr Tyr
            355                 360                 365

Ser Ser Gly Trp Trp Phe Asp Ser Cys Leu Ser Ala Asn Leu Asn Gly
    370                 375                 380

Lys Tyr Tyr His Gln Lys Tyr Lys Gly Val Arg Asn Gly Ile Phe Trp
385                 390                 395                     400

Gly Thr Trp Pro Gly Ile Asn Gln Ala Gln Pro Gly Gly Tyr Lys Ser
                405                 410                 415

Ser Phe Lys Gln Ala Lys Met Met Ile Arg Pro Lys Asn Phe Lys Pro
            420                 425                 430
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